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- c) a DNA region involved in transcription termination and polyadenylation.

EZ 11. (Amended) The method according to claim 2, wherein said eucaryotic cell is a plant cell.

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22. (Amended) A eucaryotic cell, comprising a nucleic acid of interest, which is normally capable of being phenotypically expressed, further comprising a chimeric DNA molecule comprising the following operably linked parts:

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- a) a promoter, operative in said eucaryotic cell;
 - b) a DNA region, which when transcribed, yields an RNA molecule with at least one RNA region with a nucleotide sequence comprising
 - i. a sense nucleotide sequence of at least 10 consecutive nucleotides having between 75 and 100% sequence identity with at least part of the nucleotide sequence of the nucleic acid of interest; and
 - ii. an antisense nucleotide sequence including at least 10 consecutive nucleotides, having between about 75% to about 100% sequence identity with the complement of said at least 10 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence; and optionally

- c) a DNA region involved in transcription termination and polyadenylation.

Please add the following new claims:

EY 39. The method of claim 2, wherein said DNA region, which when transcribed yields said RNA molecule, further comprises an intron.

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sup G 40. The method of claim 39, wherein said intron is located between the DNA region encoding said sense nucleotide sequence and the DNA region encoding said antisense nucleotide sequence.

41. The eucaryotic cell of claim 22, wherein said DNA region, which when transcribed yields said RNA molecule, further comprises an intron.

sup G n 42. The eucaryotic cell of claim 41, wherein said intron is located between the DNA region encoding said sense nucleotide sequence and the DNA region encoding said antisense nucleotide sequence.
